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The microbiome of biogas reactors treating lignocellulosic substrates revealed different mechanisms for carbohydrates utilization

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Abstract

The present study dissected the microbiome of biogas reactors treating lignocellulosic substrate and swine manure by means of high throughput Illumina sequencing. A comparative metagenomic analysis allowed to identify the microbial species firmly attached to the digested lignocellulosic particles and to distinguish them from the planktonic microbes floating in the liquid medium. *Proteobacteria* and *Firmicutes* were the most abundant phyla identified respectively in the liquid samples and firmly attached to the grass, and accounted approximately 17 and 22% of the total microbial counts. Additionally, *Actinobacteria* were also presented in both samples but in lower relative abundance. Assembly of the shotgun reads followed by a binning process led to the extraction of 151 genome bins, out of which 80 microbial species were completely new and not previously deposited in any database. Moreover, it was shown that 25 microbial genomes were more enriched (>2 fold) in the firmly attached grass samples compared to the liquid phase. A bioinformatic approach based on multiple databases for functional annotation (KEGG, COG, SEED and dbCAN) demonstrated that these microbial species encode enzymes related to carbohydrate utilisation and present numerous carbohydrate binding modules. Finally, it was found that apart from the cellulosome multi-enzyme complex, specific microbes, such as *Bacteroidetes*, present different mechanisms for binding and degrading the lignocellulose due to the presence of multiple CBM6 modules in beta-xylosidase and endoglucanase proteins or SLH modules in unknown proteins.